

Supplemental Information.

Materials and methods for Figure S1.

The acidobacterial 16S rRNA genes were extracted from publicly available genomes and from genomes from this study and were aligned by the SINA online tool (Pruesse *et al.*, 2012). For the phylogenetic inference of the 16S rRNA gene, additional outgroup sequences were downloaded from the SILVA SSU 128 database (Quast *et al.*, 2013). The final alignment contained 48 sequences with a minimum sequence length of 1248 nucleotides. The alignment was inspected in SeaView version 4.6.1 (Gouy *et al.*, 2010). A maximum likelihood (ML) based inference of the 16S rRNA gene tree was calculated by RAxML version 8.2.9 (Stamatakis, 2014), using the general time-reversible substitution model under the gamma model of rate heterogeneity (GTRGAMMA). 50 ML trees were generated and 1000 bootstrap replicates were computed to draw bipartitions on the best ML tree. The outgroup consists of a diverse collection of 16S rRNA gene sequences, including deltaproteobacterial sequences and Aminicenantes/OP8 sequences.

References:

- Gouy, M., Guindon, S., and Gascuel, O. (2010) SeaView Version 4: a multiplatform graphical user interface for sequence alignment and phylogenetic tree building. *Molecular Biology and Evolution* **27**: 221–224.
- Pruesse, E., Peplies, J., and Glockner, F.O. (2012) SINA: Accurate high-throughput multiple sequence alignment of ribosomal RNA genes. *Bioinformatics* **28**: 1823–1829.
- Quast, C., Pruesse, E., Yilmaz, P., Gerken, J., Schweer, T., Yarza, P., *et al.* (2013) The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. *Nucleic Acids Res.* **41**: D590–D596.
- Stamatakis, A. (2014) RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics* **30**: 1312–1313.

Table S1. Genomes used in this study including isolation source of strains and associated references.

	Reference	Environment	Abbreviations used in this study	GenBank Accession Number	NCBI Genome ID	GenBank Assembly Accession	IMG Genome ID
Subdivision 1							
<i>Terriglobus roseus</i> KBS 63 ³	this study	grassland soil ¹	KBS 63	CP003379.1	3572	GCA_000265425.1	2510461070
<i>Terriglobus</i> sp. TAA 43	this study	termite hindgut ¹	TAA 43	JUGR00000000.1	18239	GCA_000800015.1	2585428133
<i>Acidobacteriaceae bacterium</i> KBS 89	this study	grassland soil ¹	KBS 89	ARME00000000.1	30243	GCA_000381605.1	2522125061
<i>Acidobacteriaceae bacterium</i> KBS 146	this study	grassland soil ¹	KBS 146	JHVA00000000.1	31960	GCA_000688615.1	2556793019
<i>Acidobacteriaceae bacterium</i> TAA 166	this study	termite hindgut ¹	TAA 166	ATWD00000000.1	30011	GCA_000421065.1	2524614882
<i>Acidobacteriaceae bacterium</i> KBS 83	this study	agricultural soil ¹	KBS 83	ARMD00000000.1	30242	GCA_000381585.1	2519899651
<i>Acidobacterium capsulatum</i> ATCC51196 ³	(1)	acid mine drainage ²	Acap	CP001472.1	1086	GCA_000022565.1	643692001
<i>Granulicella tundricola</i> MP5ACTX9 ³	(2, 3)	tundra soil ¹	Grtund	CP002480.1	13764	GCA_000178975.2	649633002
<i>Granulicella mallensis</i> MP5ACTX8 ³	(2, 3)	tundra soil ¹	Grmall	CP003130.1	2833	GCA_000178955.2	2503982037
<i>Acidobacterium ailauui</i> PMMR2	(4)	geothermally-heated Hawaiian microbial mat ²	Aaila	JIAL00000000.1	13755	GCA_000688455.1	2558860986
" <i>Candidatus</i> Koribacter versatilis" Ellin345 ³	(1)	pasture soil ¹	Ellin 345	CP000360	1384	GCA_000014005.1	2606217699
<i>Edaphobacter aggregans</i> DSM19664	With permission KMG-I project, (N.Kyrpides)	forest soil ¹	Eaggr	JQKI00000000.1	33197	GCA_000745965.1	2571042012
<i>Silvibacterium bohemicum</i> S15	(5)	coniferous soil ¹	Silvib	LBHJ00000000.1	38174	GCA_001006305.1	2654587641

<i>Terracidiphilus gabretensis</i> S55	(6)	forest soil ¹	Tgab	LAIJ00000000.1	41667	GCA_001449115.1	2648501865
<i>Terriglobus saanensis</i> SP1PR4 ³	(3, 7)	tundra soil ¹	Tsaan	CP002467.1	2908	GCA_000179915.2	649633100
Subdivision 3							
<i>Acidobacteria bacterium</i> KBS 96	this study	agricultural soil ¹	KBS 96	ARMF00000000.1	30244	GCA_000381625.1	2522125054
<i>Bryobacter aggregatus</i> MPL3	this study	acidic Sphagnum peat bog ¹	Bryagg	JNIF00000000.1	32097	GCA_000702445.1	2562617048
<i>"Candidatus Solibacter usitatus"</i> Ellin6076 ³	(1)	pasture soil ¹	Ellin 6076	CP000473	1167	GCA_000014905.1	639633060
Subdivision 4							
<i>Chloracidobacterium thermophilum</i> B ³	(8)	alkaline microbial mats ²	Chlortherm	CP002514.1, CP002515.1	10823	GCA_000226295.1	2512047033
<i>Pyrinomonas methylaliphatogenes</i> K22	(9)	geothermal soil ²	Pyrmet	CBXV000000000	35807	GCA_000820845.2	2645727641, 2545824503
Subdivision 6							
<i>Luteitalea pratensis</i> DSM100886 ³	(10)	German soil ¹	Lprat	CP015136	44495	GCA_001618865.1)	2687453111
Subdivision 8							
<i>Geothrix fermentans</i> DSM14018	With permission KMG-I project, (N.Kyrpides)	hydrocarbon-contaminated aquifer ²	Gferm	NZ_AUAU000000000	11064	GCA_000428885.1	2523231062
<i>Holophaga foetida</i> TMBS4	(11)	anoxic freshwater mud ²	Hfoet	AGSB000000000	10811	GCA_000242615.3	2509601028
Subdivision 23							
<i>Thermoanaerobaculum aquaticum</i> MP-01	(12)	freshwater hot spring ²	Thermaq	JMFG000000000	31925	GCA_000687145.1	2579778550

¹These genomes were defined as 'soil' environments stemming from temperate (grassland, agricultural, peat, coniferous and forest soils) and Arctic soils. They are referred to in the text as 'soil'. The 'termite associated acidobacteria' were placed in this category as preliminary data suggests that are not autochthonous to the guts, rather zymogenous inhabitants of the gut (13).

²These genomes were defined as 'non temperate or Arctic soil' environments stemming from anoxic mud, hot spring, contaminated aquifer, geothermal soil, alkaline or thermophilic microbial mats, and acid mine drainage referred to in the text as "other".

³Indicates a closed genome.

References:

1. Ward N.J., Challacombe J.F., Janssen P.H., Henrissat B., Coutinho P.M., Wu M., *et al.* (2009) Three genomes in the phylum *Acidobacteria* provide insight into their lifestyles in soils. *Appl Environ Microbiol* **74**:2046–2056.
2. Rawat S.R., Mannisto M.K., Starovoytov V., Goodwin L., Nolan M., Hauser L., *et al.* (2014) Complete genome sequence of *Granulicella tundricola* type strain MP5ACTX9(T), an *Acidobacteria* from tundra soil. *Stand Genomic Sci* **9**:449–461.
3. Rawat S.R., Mannisto M.K., Bromberg Y., Haggblom M.M. (2012) Comparative genomic and physiological analysis provides insights into the role of *Acidobacteria* in organic carbon utilization in Arctic tundra soils. *FEMS Microbiol Ecol* **82**:341–355.
4. Myers M.R. and King G.M. (2016) Isolation and characterization of *Acidobacterium ailaui* sp. nov., a novel member of *Acidobacteria* sub-division I, from a geothermally-heated Hawaiian microbial mat. *Int J Syst Evol Microbiol* **66**: 5328-5335
5. Lladó S., Benada O., Cajthaml T., Baldrian P., García-Fraile P. (2016) *Silvibacterium bohemicum* gen. nov. sp. nov., an acidobacterium isolated from coniferous soil in the Bohemian Forest National Park. *Syst Appl Microbiol* **39**:14–19.
6. García-Fraile P., Benada O., Cajthaml T. (2016) *Terracidiphilus gabretensis* gen. nov., sp. nov., an abundant and active forest soil acidobacterium important in organic matter transformation. *Appl Env Microbiol* **82**:560-569.
7. Rawat S.R., Mannisto M.K., Starovoytov V., Goodwin L., Nolan M., Hauser L., *et al.* (2012) Complete genome sequence of *Terriglobus saanensis* type strain SP1PR4(T), an *Acidobacteria* from tundra soil. *Stand Genomic Sci* **7**:59–69.
8. Garcia Costas A.M., Liu Z., Tomsho L.P., Schuster S.C., Ward D.M., Bryant D.A. (2012) Complete genome of Candidatus *Chloracidobacterium thermophilum*, a chlorophyll-based photoheterotroph belonging to the phylum *Acidobacteria*. *Environ Microbiol* **14**:177–190.
9. Greening C., Carere C.R., Rushton-Green R., Harold L.K., Hards K., Taylor M.C., *et al.* (2015) Persistence of the dominant soil phylum *Acidobacteria* by trace gas scavenging. *Proc Natl Acad Sci USA* **112**:10497–10502.
10. Huang S., Vieira S., Bunk B., Riedel T., Spröer C., Overmann J. (2016) First complete genome sequence of a subdivision 6 acidobacterium strain. *Genome Announ* **4**:e00469–16.
11. Anderson I., Held B., Lapidus A., Nolan M., Lucas S., Tice H., *et al.* (2012) Genome sequence of the homoacetogenic bacterium *Holophaga foetida* type strain (TMBS4(T)). *Stand Genomic Sci* **6**:174–184.
12. Stamps B.W., Losey N.A., Lawson P.A., Stevenson B.S. (2014) Genome sequence of *Thermoanaerobaculum aquaticum* MP-01T, the first cultivated member of *Acidobacteria* subdivision 23, isolated from a hot spring. *Genome Announ* **2**:e00570–14–e00570–14.

13. Stevenson B.S., Eichorst S.A., Wertz J.T., Schmidt T.M., Breznak J.A. (2004) New strategies for cultivation and detection of previously uncultured microbes. *Appl Environ Microbiol* **70**:4748–4755.

Table S2. General genome features across new genomes from this study.

	<i>Terriglobus roseus</i>	<i>Terriglobus</i> sp.	<i>Acidobacteriaceae bacterium</i>	<i>Acidobacteriaceae bacterium</i>	<i>Acidobacteriaceae bacterium</i>	<i>Acidobacteriaceae bacterium</i>	<i>Bryobacter aggregantus</i>	<i>Acidobacteria bacterium</i>
Strain	KBS 63	TAA 43	KBS 89	KBS 83	TAA 166	KBS 146	MPL3	KBS 96
Subdivision	1	1	1	1	1	1	3	3
<i>Genome data</i>								
Genome size (bp)	5 227 858	4 947 033	6 009 926	6 250 814	6 136 933	5 001 037	5 747 993	6 692 160
DNA coding region (bp)	4 688 148	4 525 334	5 322 921	5 470 371	5 398 159	4 489 703	5 399 614	6 053 597
G+C content (mol%)	60	57	58	59	59	57	58	57
Total number of genes	4399	4262	5119	5491	5364	4230	5126	5779
Pseudogenes	92	37	110	0	254	88	144	240
RNA genes								
tRNA genes	53	47	49	47	48	49	51	71
rRNA genes	6	3	3	3	3	3	6	6
No. rRNA operons	2	1	1	1	1	1	2	2
Other RNA genes	2	4	4	5	6	5	4	7
<i>Total protein CDSs (%)</i>								
With function prediction (%)	3220(73.2)	3141(73.7)	3605(70.42)	3755(68.38)	3837(71.53)	3209(75.86)	3684(71.87)	4193(71.52)
With COGs (%)	2557(58.13)	2465(57.84)	2802(54.74)	2841(51.74)	2975(55.46)	2586(61.13)	2781(54.25)	3214(54.82)
With Pfam domains	3,351(76.18)	3248(76.21)	3,785(73.94)	3,914(71.28)	3963(73.88)	3325(78.61)	3819(74.5)	4357(74.31)
Coding for signal peptides (%)	765(17.39)	808(18.96)	800(15.63)	744(13.55)	648(12.08)	670(15.84)	612(11.94)	718(12.25)
Coding for transmembrane proteins (%)	1097(24.94)	1034(24.26)	1344(26.26)	1420(25.86)	1233(22.99)	1059(25.04)	1043(20.35)	1364(23.26)

Table S3. Genome completeness, contamination and strain heterogeneity across all investigated genomes based on CheckM.

Species/Genome	Genome Assembly	Size (Mb)	GC (%)	Genes	Proteins	Completeness (%)	Contamination (%)	Strain Heterogeneity (%)
Subdivision 1								
<i>Terriglobus roseus</i> KBS 63*	GCA_000265425.1	5.23	60.3	4319	4176	100	13.79	94.44
<i>Terriglobus</i> sp. TAA 43	GCA_000800015.1	4.95	56.7	4178	4079	100	2.59	0
<i>Acidobacteriaceae</i> bacterium KBS 89	GCA_000381605.1	6.01	57.6	4992	4835	100	0.86	0
<i>Acidobacteriaceae</i> bacterium KBS 146	GCA_000688615.1	5.00	56.7	4124	3989	100	0	0
<i>Acidobacteriaceae</i> bacterium TAA 166	GCA_000421065.1	6.14	58.8	5161	4975	99.14	4.48	0
<i>Acidobacteriaceae</i> bacterium KBS 83	GCA_000381585.1	6.25	59.2	5273	5079	99.14	0	0
<i>Acidobacterium capsulatum</i> ATCC51196*	GCA_000022565.1	4.13	60.5	3396	3281	100	0.85	0
<i>Granulicella tundricola</i> MP5ACTX9*	GCA_000178975.2	5.50	59.9	4687	4542	99.15	0.85	0
<i>Granulicella mallensis</i> MP5ACTX8*	GCA_000178955.2	6.24	57.9	4844	4735	99.14	2.63	0
<i>Acidobacterium ailaoui</i> PMMR2	GCA_000688455.1	3.69	56.5	3159	3043	100	0	0
" <i>Candidatus</i> Koribacter versatilis" Ellin345*	GCA_000014005.1	5.65	58.4	4972	4860	99.95	0	0
<i>Edaphobacter aggregans</i> DSM19664	GCA_000745965.1	8.18	58.7	7121	6610	100	1.72	0
<i>Silvibacterium bohemicum</i> S15	GCA_001006305.1	6.46	58.2	5292	5117	100	3.85	0
<i>Terracidiphilus gabretensis</i> S55	GCA_001449115.1	5.35	57.3	4386	4244	99.78	0.86	0
<i>Terriglobus saanensis</i> SP1PR4*	GCA_000179915.2	5.10	57.3	4261	4163	100	1.72	0
Subdivision 3								
<i>Acidobacteria</i> bacterium KBS 96	GCA_000381625.1	6.69	57.2	5746	5567	97.39	0.87	0
<i>Bryobacter aggregatus</i> MPL3	GCA_000702445.1	5.75	57.9	5051	4918	98.26	1.74	0
" <i>Candidatus</i> Solibacter usitatus" Ellin6076*	GCA_000014905.1	9.97	61.9	8113	7991	100	0.88	0
Subdivision 4								
<i>Chloracidobacterium thermophilum</i> B*	GCA_000226295.1	3.69	61.3	3034	2905	95.71	2.56	0
<i>Pyrinomonas methylaliphatogenes</i> K22	GCA_000820845.2	3.79	59.4	3216	3067	96.53	1.71	0
Subdivision 6								
<i>Luteitalea pratensis</i> DSM100886*	GCA_001618865.1	7.48	67.2	6293	6200	97.44	5.13	16.67
Subdivision 8								
<i>Geothrix fermentans</i> DSM 14018	GCA_000428885.1	3.29	68.9	2925	2806	99.12	0	0
<i>Holophaga foetida</i> TMBS4	GCA_000242615.3	4.13	62.9	3581	3471	99.12	0.88	0
Subdivision 23								
<i>Thermoanaerobaculum aquaticum</i> MP-01	GCA_000687145.1	2.66	63.0	2393	2251	94.44	1.71	0

*denotes a closed genome.

Table S4. Preliminary assessment of putative insertion sequence (IS) element families across the acidobacterial genomes. Abbreviations for the genomes can be found in Table S1. Numbers represent complete/partial/pseudogene/unknown IS elements. Analysis was performed using the ISsaga – IS Semi-automatic genomic annotation website (http://issaga.biotoul.fr/issaga_login.php?type=2). Putative IS elements need to be manually curated.

IS element families	Acap	A.aillaaui	Gtund	Gmall	Ellin345	TAA43	Tsaan	KBS63	KBS146	Edapho	TAA166	KBS83	KBS89	Silvib	Tgab	Ellin6076	KBS96	MPL3	Chloroacd	K22	Lprat	Hfoet	Gferm	Thermana
IS1182				0,0,0,1		1,0,0,0	0,1,0,0			0,4,0,2	3,0,0,0	0,2,0,0			0,0,0,1	0,0,0,1	0,1,0,0				0,1,0,7			
ISNCY_ssg IS1202									0,1,0,0	3,14,0,5				1,0,0,0		0,0,0,4	2,0,0,0							0,1,0,1
IS66			0,1,0,1				0,2,0,1			2,2,0,6				2,4,0,2		1,0,0,1	0,3,0,0	2,1,0,2						
IS701										0,6,0,6						1,0,0,9								
IS630										4,13,0,10					1,0,0,0	1,1,0,6		10,5,0,14			3,7,0,1			
ISL3	0,0,0,2	0,0,0,2	2,1,0,1	0,0,0,2	0,0,0,2	0,0,0,1	0,2,0,5	0,2,0,7	0,1,0,8	0,4,0,7	1,0,0,0	0,2,0,2			0,0,0,3	1,4,0,2	0,0,0,4	0,1,0,2	0,0,0,2	0,1,0,3		1,1,0,5	0,5,0,1	
IS481	11,1,0,1		1,0,0,0	1,0,0,2					0,1,0,1	1,5,0,3	0,3,0,0	0,0,0,1		0,2,0,0	1,0,0,1	12,0,0,1		9,3,0,1		0,0,0,1	4,0,0,0		0,15,0,0	0,1,0,0
IS3_ssg IS3	0,0,0,1									1,2,0,0						15,0,0,14								
IS110	2,0,0,0	1,2,0,1		2,4,0,0						2,19,0,15			0,5,0,0	1,0,0,0	0,2,0,0	18,0,0,3	1,3,0,5	0,0,0,1			1,0,0,3		0,1,0,1	
IS6										3,6,0,2	0,1,0,0	0,2,0,1				3,4,0,0								
IS91										6,13,0,12						4,1,0,6	0,2,0,0						3,0,0,9	
IS21	3,3,0,3	1,0,0,1								2,7,0,3						5,1,0,3	3,6,0,2					7,2,0,3	8,0,0,3	
IS3_ssg IS407	5,2,0,0	4,2,0,0	0,3,0,0	0,1,0,1			0,1,0,0			5,12,0,2	21,12,0,2			1,9,0,3	2,4,0,0		0,0,0,2	2,0,0,0						
IS5				4,0,0,0						0,2,0,0				0,0,0,1			0,1,0,0							
IS3_ssg IS3										0,1,0,1							0,1,0,0					1,1,0,0		
IS630		0,1,0,0								0,5,0,4							0,1,0,2			0,0,0,2		0,0,0,1		
IS110_ssg IS111		1,0,0,2	7,0,0,0	1,0,0,1	5,0,0,2		3,2,0,0	0,4,0,0		2,21,0,5	3,2,0,0	0,2,0,6		0,1,0,1			3,0,0,1				0,0,0,3			

IS element families	Acap	A.aillaaui	Gtund	Gmall	Ellin345	TAA43	Tsaan	KBS63	KBS146	Edapho	TAA166	KBS83	KBS89	Silvi b	Tgab	Ellin6076	KBS96	MPL3	Chloroacd	K22	Lprat	Hfoet	Gferm	Thermana
IS256		0,1,0,5															5,0,0,2			0,12,0,0	3,0,0,0			
IS4_ssgr_IS4Sa										0,3,0,1														
IS3_ssgr_IS51																								
IS5_ssgr_IS1031										3,8,0,4														
IS5_ssgr_IS427	3,0,0,0									3,2,0,3	1,2,0,0	2,4,0,5		3,5,0,1									1,0,0,1	
IS5_ssgr_IS5	1,2,0,0	0,3,0,0	16,4,0,0							2,17,0,0		0,2,0,0	0,1,0,0											
ISNCY_ssgr_ISPlu15																				0,0,0,2				
IS200_IS605		2,1,0,0																		0,1,0,1	2,0,0,1			
IS200_IS605_ssgr_IS1341																				0,2,0,1	0,0,0,10			
IS607																				3,1,0,0	2,0,0,0			
ISAs1										0,3,0,3	1,0,0,0												6,0,0,0	
IS1595_ssgr_ISPna2																					0,0,0,1			
IS66_ssgr_ISBst12																							0,0,0,12	
IS1380										0,1,0,14													1,0,0,0	
ISNCY_ssg_ISLbi1																							1,0,0,0	0,2,0,0
IS1634																							1,2,0,2	
IS200_IS605_ssgr_IS200				0,0,0,1		0,0,0,2		0,0,0,2		1,0,0,0													2,2,0,0	
IS1595_ssgr_IS1595										0,0,0,1													5,1,0,1	
IsoAzo_13										0,0,0,4													0,0,0,2	0,0,0,1

Table S5. Locus tag for the genes identified across the acidobacterial genomes encoding for the catalytic subunit of respiratory oxygen reductases (cytochrome terminal oxidases). Locus tags for each gene starts with the ID given in column “locus tag start”, followed by the number in the respective column.

Genome	Locus tag			
	Locus tag start	HCO ¹ type A	HCO ¹ type C	<i>bd</i> cytochrome oxidase
<i>“Candidatus Koribacter versatilis”</i> Ellin345	Acid345_	2995 0438	ND	3252
<i>Terriglobus saanensis</i> SP1PR4	AciPR4_	0757 1977 1384 4039 1735	ND	ND
<i>Terriglobus roseus</i> KBS 63	Terro_	0292 4044	4248	ND
<i>Terriglobus</i> sp. TAA 43	M504DRAFT_	1755 2704 1876	ND	ND
<i>Granulicella mallensis</i> MP5ACTX8	AciX8_	1358 0184 2887	ND	2831
<i>Granulicella tundricola</i> MP5ACTX9	AciX9_	0075 1502 2163	ND	ND
<i>Acidobacteriaceae bacterium</i> KBS 89	G003DRAFT_	1427 1559 2097	ND	ND
<i>Acidobacteriaceae bacterium</i> KBS 146	M015DRAFT_	2746	ND	0063
<i>Acidobacteriaceae bacterium</i> TAA 166	H979DRAFT_	2562 4938	ND	5221 0828 (fragmented)
<i>Edaphobacter aggregans</i> DSM 19364	Q363DRAFT_	00800 00183 03851 06175 01386	03854 03822	01553 04806 (only 113 aa)
<i>Terracidiphilus gabretensis</i> S55	Ga0102063_	1091461 109341	ND	ND
<i>Acidobacteriaceae bacterium</i> KBS 83	G002DRAFT_	03417 03882 04166 04897	ND	ND
<i>Acidobacterium capsulatum</i> ATCC 51196	ACP_	2437	0885	0468

Genome/Strain	Locus tag			
	Locus tag start	HCO ¹ type A	HCO ¹ type C	bd cytochrome oxidase
<i>Silvibacterium bohemicum</i> S15	Ga0077217_	10214 10884 102165 103529	ND	103203 103592
<i>Acidobacterium ailaui</i> PMMR2	N655DRAFT_	2211 1168 0997	1334	0369 1326
" <i>Candidatus Solibacter usitatus</i> " Ellin6076	Acid_	5590 0498 7581 6908	3507	6681
<i>Acidobacteria bacterium</i> KBS 96	G004DRAFT_	1132 1673 5485 4385	0635	ND
<i>Bryobacter aggregatus</i> MPL3	M017DRAFT_	4951 4036	ND	ND
<i>Chloracidobacterium thermophilum</i> B	Cabther_	B0233	ND	A0912
<i>Pyrinomonas methylaliphatogenes</i> K22	Ga0098325_	108284	ND	10780
<i>Luteitalea pratensis</i> DSM100886	Ga0133452_	11386 115325	114699	115305
<i>Holophaga foetida</i> DSM 6591	HolfoDRAFT_	0900	ND	1360
<i>Geothrix fermentans</i> DSM 14018	G398DRAFT_	02716	ND	02386 00741
<i>Thermoanaerobaculum aquaticum</i> MP-01	EG19_	02365	ND	10715

¹HCO=heme-copper oxygen reductase/terminal oxidases, ND=not detected

Table S6. Marker genes identified for nitrogen metabolism across acidobacterial genomes. Columns provide the function ID (EC or TC number), product (enzyme, transporter) name, gene name and locus numbers for each genome represented by its strain name.

Function ID	Product	Gene name	SD 1														SD 3			SD 4		SD 6		SD 8		SD 23		
			Ellin 345 Acid345_	SP1PR4 AcIPR4_	KBS 63 Terro_	TAA 43 M504DRAFT_	MP5ACTX8 AcX8_	MP5ACTX9 AcX9_	KBS 89 G003DRAFT	KBS 146 M015DRAFT_	TAA 166 H979DRAFT_	DSM19364 Q363DRAFT_	S55 Ga0102063_	KBS 83 G002DRAFT_	ATCC51196 ACP_	S15 Ga0077217_	PMMR2 N655DRAFT_	Ellin6076 Acid_	KBS 96 G004DRAFT_	MPL3 M017DRAFT_	B Cabther_	K22 Ga0098325_	DSM100886 Ga0133452_	TMB54 HolloDRAFT_	DSM14018 G398DRAFT_	MP-01 EG19_		
Dissimilatory nitrate and nitrite reduction (denitrification)																												
EC:1.7.99.4	Membrane-bound nitrate reductase	<i>narG</i> operon	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	01357-01360	ND
EC:1.7.99.4	Periplasmic nitrate reductase	<i>napA</i> operon	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	12345-12365
EC:1.7.2.1	Copper-containing nitrite reductase	<i>nirk</i>	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
EC:1.7.2.2	Nitrite reductase (cytochrome; ammonia froming)	<i>nrjHA</i>	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
EC:1.7.2.5	Nitric-oxide reductase	<i>norBC/norZ</i>	0364	ND	0243	ND	ND	ND	ND	ND	103454	01282 04947	ND	ND	ND	103454	0246	7864 2936	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
EC:1.7.2.4	Nitrous-oxide reductase	<i>nosZ</i>	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Assimilatory nitrate and nitrite reduction																												
EC:1.7.99.4	Nitrate reductase	<i>nasA</i>	ND	ND	1211	3864	0895	0125	2174	0852	ND	05846	ND	ND	ND	ND	3124	0183 2928	0571 3063	ND	ND	ND	ND	ND	ND	ND	ND	ND
EC:1.7.1.15	Nitrite reductase (NADH)	<i>nirB</i>	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	0184	0570	ND	ND	ND	ND	ND	ND	ND	ND	ND
EC:1.7.7.1	Ferredoxin-nitrite reductase	<i>nirA</i>	ND	ND	1214	3867	0892	0128	2177	0855	ND	ND	ND	04105 04104	ND	ND	3127	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
TC 2.A.1.8	Nitrate/ nitrite porter (NNP)	<i>nark/ NRT</i>	ND	ND	1210	3863	0896	0124	2173	0851	0043 0694 3072	05844	ND	595	ND	ND	3123	0186 2929	3064	4414	ND	ND	ND	ND	ND	ND	ND	ND
Ammonia assimilation																												
EC:6.3.1.2	Glutamine synthetase (GS)	<i>glnA</i>	3142 0166	1794	1807	0692	1285	1375	3064	4032	3823	02162	11234	01403 04563	1250 0595	104762	2561	4831 1901 0067	2781 4790	1794 1790	A2003	104218	116176 113561	0125	01680	09235	ND	
EC:1.4.1.-13/14	Glutamate synthase (GOGAT), large chain	<i>gltB</i>	3680	2050	1714	0089	2097	1897	2498	0072	4010	01545	107121	03977	2997	119172	3103	3816	5814	0322	A1316	108822	115550	0249	00368	04200	ND	
EC:1.4.1.-13/14	Glutamate synthase (GOGAT), small chain	<i>gltD</i>	2796 3679	ND	4344	ND	2687	0264	2908	ND	ND	04267	110352	ND	1387	102335	ND	3815 0543 3510 7661	5815	0323	ND	108823 108709 113556	115549 114103	0248 2650 0142 3463 2931	01329	08420 02560	ND	
EC:1.4.1.2	Glutamate dehydrogenase (NAD) (GDH)	<i>gdh2</i>	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
EC:1.4.1.-3/4	Glutamate dehydrogenase (NAD(P)(+)/NADP(+)) (GDH)	<i>gdhA</i>	0943 2942 4115	1275	2787	0923	0803	3035	3262	3517	1094	05027	11259	02399	2883	102135	2044	0039 4761	0737 4563	0363 1312	A2079 80781	10526	ND	1742 2764	01097 01591 02884	08250	ND	
Ammonium uptake transport																												
TC 1.A.11	Ammonium transporter	<i>amtB</i>	1490 3596 4446	0992	1497	0950	4320 3327	2274	2799	4215	0572	02736	1064	03980	1255 1252 0919	101403	0634	7190 5532	0661 3003	1792	A0160	108593	113472 113167	0124 0122 3429	00569 00857	ND	ND	
-	Nitrogen regulatory protein P-II	<i>glnK</i>	1489 4445	0991	1496	0951	4321 3326	2273	2798	4216	0571	02735	1065	03979	0920	101402	0635	7189 5534	0660	1793	A0161	108595	113471	0123 0121 3428	00568 00856	ND	ND	

Table S6. Marker genes identified for nitrogen metabolism across acidobacterial genomes. Columns provide the function ID (EC or TC number), product (enzyme, transporter) name, gene name and locus numbers for each genome represented by its strain name.

Function ID	Product	Gene name	SD 1														SD 3			SD 4			SD 6		SD 8		SD 23
			Ellin 345 Acid345_	SP1PR4 AcIPR4_	KBS 63 Terro_	TAA 43 M504DRAFT_	MPSACTX8 AcX8_	MPSACTX9 AcX9_	KBS 89 G003DRAFT	KBS 146 M015DRAFT_	TAA 166 H979DRAFT_	DSM19364 Q363DRAFT_	S55 Ga0102063_	KBS 83 G002DRAFT_	ATCC51196 ACP_	S15 Ga0077217_	PMMR2 N655DRAFT_	Ellin676 Acid_	KBS 96 G004DRAFT_	MPL3 M017DRAFT_	B Cabther_	K22 Ga0098325_	DSM100886 Ga0133452_	TMBS4 HolfDRAFT_	DSM14018 G398DRAFT_	MP-01 EG19_	
Amino acid (AA) transport																											
TC 2.A.3	AA-polyamine-organocation (APC) superfamily	-	3835	1416	4224	0571	2786	3472	2480	0789	4308	02969	101130	04930	3401	103118	0731	7162	2943	3654	A0283	108537	112573	2468	00939	03995	
			3036	2037	3913	0973	1117	1886	3866	0094	4024	04137	112108	00444	1795	104794	2168	2823	0110	3019	A1466	104442	111053	0909	00553	08400	
			0162	3497	0836	4186	1565	2694	1151	0088	3310	06911	110422	01650	0121	11833	2616	2999	4012	3778	80209	108342	113432	2467	01205	07245	
			0976	2464	3040	1421	1566	3345	3528	1963	3131	01532	1091158	02984	1264	104291	1848	0814	3303	4169		10549	115635		01204		
			0678	0020	2261	0465	4112	0983	2967	3716	4700	02982	1091361	04564	0122	119163	1530	3825	2272	3168		10713	115468		02692		
			1536	2651	3794	2262	2732	2124	4692	0087	4844	02841	102161	04463	3520	11415	1461	4914	4788	2459		108598	114739				
			1679	2036	1607	1033	0955	1885	2481	3264	4422	01525	101213	02605	0855	104624	2511	5796	1038	3793		10550	11630				
			3333	0364	1744	0974	4779	3541	3361	0803	4025	00909	101180	02850	1500	103418	2510	4943	0248	4168		108850	114707				
			0046	3374	4002	2758	0411	1735	0152	0429	4714	06534	109238	03907	3151	104282	0180	2124	0923	2862		10639	115073				
			3285	0178	1745								01136	102162	01718		11416	1822	3740			112092	112092				
			2701	3964	1504								01531	102153	02065		119135	1175	2626			101308	114166				
			3016		2625								04348	10425	04646		120582	1927	4366								
			3114											1015	04042		112218	4944									
			1474														104387	4619									
3284														103119	2296												
2156														104110	1835												
3351														104225	1245												
															4783												
TC 2.A.23	Dicarboxylate/AA:cation symporter (DAACS) family	-	2088	1150	3462	1300	1251 1919	0511 2737	0046 4779	3790	0690	00653	109422	00209	ND	104275	2012	3691 1117	ND	3990	80019	107111	112162 114989	ND	01633 01569	04235	
TC 3.A.1.4.-	Branched chain hydrophobic AA (HAAT) transporter (ABC superfamily)	<i>livKFGHM</i>	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	6083	ND	ND	A0310 A0414 A0416 80208 80693	ND	ND	0334-0338 0471-0475 1865-1869 0012 0020 0049 0434 1336 1660 2091 3541	00619-00623 01283-01287 02586-02589 02014	00910 10105 10165 10890		
Nitrogen fixation																											
EC 1.18.6.1	Nitrogenase	<i>nifH</i> operon	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	0884-0892	ND	ND	
Proteases: select peptidases																											
EC:3.4.21.-	Serine endopeptidases family 58 (subtilisin-like) and family 553	-	2635 3141 4222	1724	1995 2361 2960 3758	0214 1078 1356 3807	0674 3104	0612 1366 2897	1754 4086 4513	0225 3702	3468 3298 5203	02302 03219 04118	101114 1091596	01357 03150	1810	10438 101563 114128	1743	7045 6709 5611 3452 6185 0578 3135	3271 1283 5333 2600	3675 1502 3514 2644 4202	A0104 A0163 A0211 A1826 A1515 80297	108125 108305 105147 106189 102293 108463	112415 116070 113401 111417 114755 111450 115742	ND	ND	04460 09280	
EC:3.4.24.-	Metallopeptidase family M3	-	1180	4110	1333	1014	3979 4246	2083	4538	2775	2381	00038	112387	02390	2228	11292 102128	2060	7278 5816	2784	1610	ND	ND	113238 113591	1677 3635	01094	01275	
EC:3.4.24.-	Metalloendopeptidase family M4	-	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	1179 111548	ND	00921 01202 01974	01045 11630 09070 09065	
EC:3.4.24.-	Metallopeptidase family M13	-	1078 4516 4515 1491 0009	0730 2272	3760 4203 3972	1358 2791 4565 2824 1950	3677 0774 0257 1217	4474 0774 0014 2977	0313 3212 3722 4830 0755	3575 1401 1755	5263 1241 1022	01998 02505 01905 00004 00734	10728 109506	00149 00270 00269	1917 2297 2953	101692 104479	2759	2743 1534 2789 1818 4723	2785	3320	ND	ND	115371 113880	ND	01908 01909 02780	ND	
EC:3.4.24.-	Metallopeptidase family M16	-	0622 1568 0621 4406	0158 1386	0079 1422	0170 2147	1363 1743 1364 0386	1564 4241 2145 2146	2647 4241 4242 0644	4068 4451 4069 4450 1035	4632 4451 1747 01746 03540	01998 02505 01905 00004 00734	1091689 1091688 110289 10238 10810	03532 03533 02436 02075	0056 0482	101313 101314 101280	2801 2802 1801 7201 2731 1734 5264	2456 2457 0912 3434 0913 3153 0429 3154 0430 1857 1695 2535	3433 A1433 A0775 A1066 A1254 A0625 A1967	108712 108713 10312 10313 108415 108416 10318 102335 104338 108899	11572-1/2 1128-79/80 11488-0/1 1187-4/5	2093 2493 1792	00902 00903 02791 00971	04450 04455 03040 11145			

ND = not detected

Table S7. Locus tags across the acidobacterial genomes encoding for putative genes involved in fermentation pathways.

Genome	Locus Tag						
	L-lactate dehydrogenase (<i>ldh</i> , EC 1.1.1.27)	D-lactate dehydrogenase (<i>ldhA</i> , EC 1.1.1.28)	Formate C-acetyltransferase (<i>pflD</i> , EC 2.3.1.54)	Fumarate reductase/succinate dehydrogenase (<i>frdABC/sdhCAB</i> ; EC 1.3.5.4/1.3.5.1)	Alcohol dehydrogenase (<i>adh/adhP</i> , EC 1.1.1.1)	Phosphate acetyltransferase/Phosphate butyryltransferase (<i>pta/ptb</i> , EC 2.3.1.8/19)	Acetate kinase (<i>ackA</i> , EC 2.7.2.1)
Subdivision 1							
<i>"Candidatus Koribacter versatilis"</i> Ellin345 Acid345_	1483	ND	ND	138/3-5 257/0-2	0379 3044 4584	ND	ND
<i>Terriglobus saanensis</i> SP1PR4 AciPR4_	ND	ND	ND	101/0-2	1211	ND	0488
<i>Terriglobus roseus</i> KBS 63 Terro_	ND	ND	ND	107/2-4	2197 2561	ND	3746
<i>Terriglobus</i> sp. TAA 43 M504DRAFT_	ND	ND	ND	379/5-9	1157	ND	0424
<i>Granulicella mallensis</i> MP5ACTX8 AciX8_	ND	ND	ND	1299-1303	2812	ND	1456 4385
<i>Granulicella tundricola</i> MP5ACTX9 AciX9_	ND	ND	ND	138/6-9	2541 3151 4423	ND	0152 1690
<i>Acidobacteriaceae bacterium</i> KBS 89 G003DRAFT_	0265, 3782	ND	ND	30/46-50 43/48-50	1342 3131 4445	5071	3419 5070
<i>Acidobacteriaceae bacterium</i> KBS 146 M015DRAFT_	ND	ND	ND	4046 40/49-50	1075 2521 2893	3871	2059
<i>Acidobacteriaceae bacterium</i> TAA 166 H979DRAFT_	ND	ND	ND	3837 384/0-1	1955 2301 5366	ND	2034

<i>Edaphobacter aggregans</i> DSM19664 Q363DRAFT_	ND	ND	03979	0107/0-2 049/39-41 02176 021/79-81	00158 03835 05534 07321	03981	00865 03980 06211 06561
<i>Terracidiphilus gabretensis</i> S55 Ga0102063_	ND	ND	ND	10235/5-8	102323	107253	10232 10454
<i>Acidobacteriaceae bacterium</i> KBS 83 G002DRAFT_	ND	ND	ND	0190/3-5 0275/6-8 0417/7-9	02395 04049	ND	00108 03488
<i>Acidobacterium capsulatum</i> ATCC51196 ACP_	ND	ND	ND	010/1-3	0589 3493	0481	2233
<i>Silvibacterium bohemicum</i> S15 Ga0077217_	ND	ND	ND	10816/5-7	101678 103210 103237 120454	ND	10390 103263 104206
<i>Acidobacterium ailaui</i> PMMR2 N655DRAFT_	ND	ND	ND	298/0-2	0373 2477	ND	0172
Subdivision 3							
<i>"Candidatus Solibacter usitatus"</i> Ellin6076 Acid_	ND	ND	ND	740/1-3	1558 5165 7928	1084 1330	3041 3255
<i>Acidobacteria bacterium</i> KBS 96 G004DRAFT_	ND	ND	ND	04/19-21	4761 5084 5508	ND	4429 5598
<i>Bryobacter aggregatus</i> MPL3 M017DRAFT_	ND	0131	ND	33/48-50	0776 4021 4026	ND	1118
Subdivision 4							
<i>Chloracidobacterium thermophilum</i> B Cabther_	A0304	ND	ND	A055/2-5	A1652 B0535	A1909	B0746
<i>Pyrinomonas methylaliphato</i> genes K22 Ga0098325_	ND	ND	ND	10416/4-6	102184	108767	108839

Subdivision 6							
<i>Luteitalea pratensis</i> DSM100886 Ga0133452_	ND	111066	112212	1139/61-64 (frdABCD) 11415/2-4 1163/3-5	111091 112028 113099 115686	112214	112213
Subdivision 8							
<i>Holophaga foetida</i> TMBS4 HolfoDRAFT_	ND	ND	ND	045/6-8	3261	0402 1130	1418 3547
<i>Geothrix fermentans</i> DSM14018 G398DRAFT_	ND	01384	ND	0044/5-7	ND	00176 00396	00464
Subdivision 23							
<i>Thermoanaerobaculum aquaticum</i> MP-01 EG19_	ND	ND	ND	079/45-55	04475	06665	03040

ND = not detected

ND: EC 1.1.2.3; L-lactate dehydrogenase (cytochrome): *lldD*

Table S8. Locus tags for the genes identified across the acidobacterial genomes encoding for genes involved in heterotrophic carbon dioxide fixation. The complete locus tags for each genome are listed.

Genome	Locus Tag				
	Phosphoenolpyruvate carboxylase (EC:4.1.1.32)	Phosphoenolpyruvate carboxylase (EC:4.1.1.49)	Isocitrate dehydrogenase (EC:1.1.1.42)	2-ketoglutarate ferredoxin oxidoreductase (EC:1.2.7.3)	Pyruvate ferredoxin oxidoreductase (EC:1.2.7.1)
Subdivision 1					
<i>"Candidatus Koribacter versatilis"</i> Ellin345	Acid345_0537	ND	Acid345_1950	Acid345_0598, 0599, 0951, 0952, 1808, 1809, 1810, 1811	Acid345_0730
<i>Terriglobus saanensis</i> SP1PR4	AciPR4_0804	ND	AciPR4_1000	ND	ND
<i>Terriglobus roseus</i> KBS 63	Terro_4338	ND	Terro_0474,0475	ND	ND
<i>Terriglobus</i> sp. TAA 43	M504DRAFT_3277	ND	M504DRAFT_1564,1565	ND	ND
<i>Granulicella mallensis</i> MP5ACTX8	AciX8_0596	ND	AciX8_1286	ND	ND
<i>Granulicella tundricola</i> MP5ACTX9	AciX9_2691	ND		ND	ND
<i>Acidobacteriaceae bacterium</i> KBS 89	G003DRAFT4411	ND	G003DRAFT3061	G003DRAFT1319, 1320, 4283, 4284	ND
<i>Acidobacteriaceae bacterium</i> KBS 146	M015DRAFT_1423	ND	M015DRAFT_4036	ND	ND
<i>Acidobacteriaceae bacterium</i> TAA 166	H979DRAFT_4777	ND	H979DRAFT_3827	ND	ND
<i>Edaphobacter aggregans</i> DSM19664	Q363DRAFT_00717	ND	Q363DRAFT_02165	ND	ND
<i>Terracidiphilus gabretensis</i> S55	Ga0102063_1017	ND	Ga0102063_112310	Ga0102063_101309, 101310	Ga0102063_10929
<i>Acidobacteriaceae bacterium</i> KBS 83	ND	G002DRAFT_02415	G002DRAFT_02770	G002DRAFT_04297, 04298	ND
<i>Acidobacterium capsulatum</i> ATCC51196	ND	ACP_2868	ACP_0089,0990	ACP_0328, 0329	ACP_2686
<i>Silvibacterium bohemicum</i> S15	ND	Ga0077217_102148	Ga0077217_103872	Ga0077217_120586, 120587	ND
<i>Acidobacterium ailaoui</i> PMMR2	ND	N655DRAFT_2950	N655DRAFT_2813	N655DRAFT_0140, 0141	ND
Subdivision 3					
<i>"Candidatus Solibacter usitatus"</i> Ellin6076		Acid_1079, 3468	Acid_2824	Acid_1871, 1872, 6987, 6988, 6989, 6990, 7692, 7693	Acid_6996

<i>Acidobacteria bacterium</i> KBS 96	G004DRAFT_5151 & 5153	ND	G004DRAFT_2333	ND	ND
<i>Bryobacter aggregatus</i> MPL3	ND	M017DRAFT_1799	M017DRAFT_2772	ND	ND
Subdivision 4					
<i>Chloracidobacterium thermophilum</i> B	ND	Cabther_A0695	Cabther_A1903	Cabther_B0326, B0327	ND
<i>Pyrinomonas methylaliphatogenes</i> K22	ND	Ga0098325_108216	Ga0098325_108311	ND	ND
Subdivision 6					
<i>Luteitalea pratensis</i> DSM100886	Ga0133452_112042	ND	Ga0133452_114156	Ga0133452_114148, 114149	Ga0133452_114104
Subdivision 8					
<i>Holophaga foetida</i> TMBS4	ND	ND	HolfoDRAFT_3426	HolfoDRAFT_0146, 0147, 3365	HolfoDRAFT_0066, 0241, 0242, 0243, 0244
<i>Geothrix fermentans</i> DSM14018	ND	ND	G398DRAFT_00282	G398DRAFT_00715, 00716, 02143, 02144, 02484	G398DRAFT_01330
Subdivision 23					
<i>Thermoanaerobaculum aquaticum</i> MP-01	ND	EG19_12120	EG19_08945	EG19_09710, 09715, 09720, 09725, 09950	EG19_02555, 02570, 04855

“ND” – not detected.

Table S9. Locus tag for the putative genes along with genome ID identified across the acidobacterial genomes associated with the group 1h/5 [NiFe]-hydrogenases. Locus tags for each gene starts with “locus tag start”, followed by the number in the respective column.

Gene name	<i>Acidobacteriaceae bacterium</i> KBS 83 (G002DRAFT)	<i>Edaphobacter aggregans</i> DSM19364 (Q363DRAFT)	<i>Granulicella mallensis</i> MP5ACTX8 (AciX8)	<i>Acidobacterium bacterium</i> KBS 96 (G004DRAFT)	“ <i>Ca. Solibacter usitatus</i> ” Ellin6076 (Acid)	<i>Pyrinomonas methylaliphatogenes</i> K22 (Ga0098325)
<i>Catalytic subunits</i>						
hhyS	0345	01013	4213	3346	6923,6925	108803
hhyL	0346	01012	4214	3345	6926	108804
HP				3344		
<i>Unknown proteins</i>						
FeS protein	03437	01011	4215	3343	6924	108805
HP	03438	01010	4216	3342	ND	108806
HP	03439	01009	4217	3341	ND	108807
HP	03440	01008	4218	3340	ND	108808
HP	ND	ND	4219	ND	ND	108809
<i>Maturation protease</i>						
HupD	03441	01007	4220	3339	6927	108810
<i>hypABCDEFGF, hydrogenase maturation proteins</i>						
HypA	03448	01000	4222	3331	6923	108813
HypB	03449	00999	4223	3330	6932	108814
HypC	03442	01006	4210	3337	6928	108815
HP	ND	ND	4221	ND	6933	108816
HypD	03443	01005	4211	3336	6929	108817
HypE	03444	01004	4212	3335	6930	108818
GmhA	03445	01003	ND	3334	ND	108819
GrxC	03446	01002	ND	3333	ND	108820
HypF	03447	01001	4209	3332	6931	108821

ND = indicates either the gene was not identified.

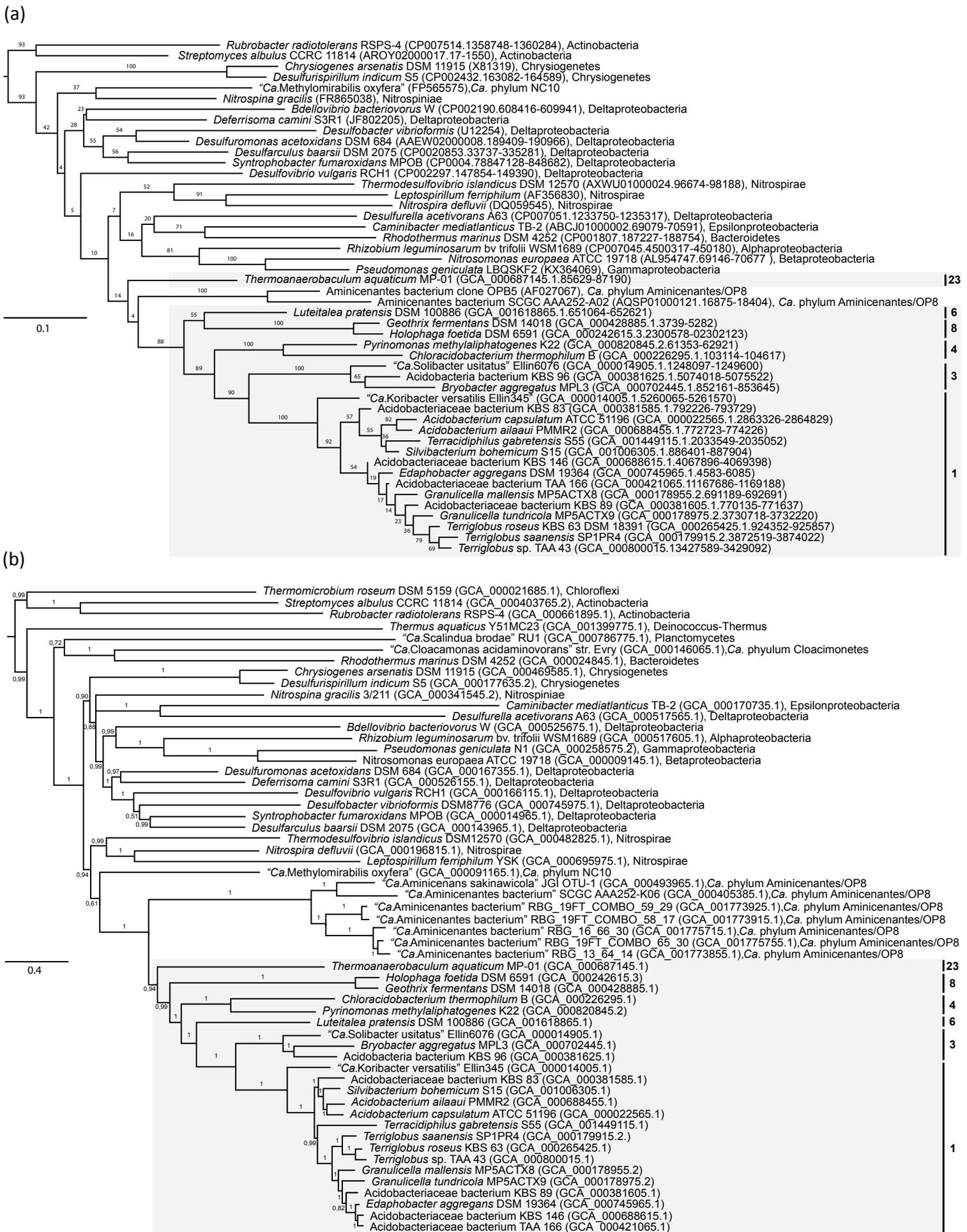
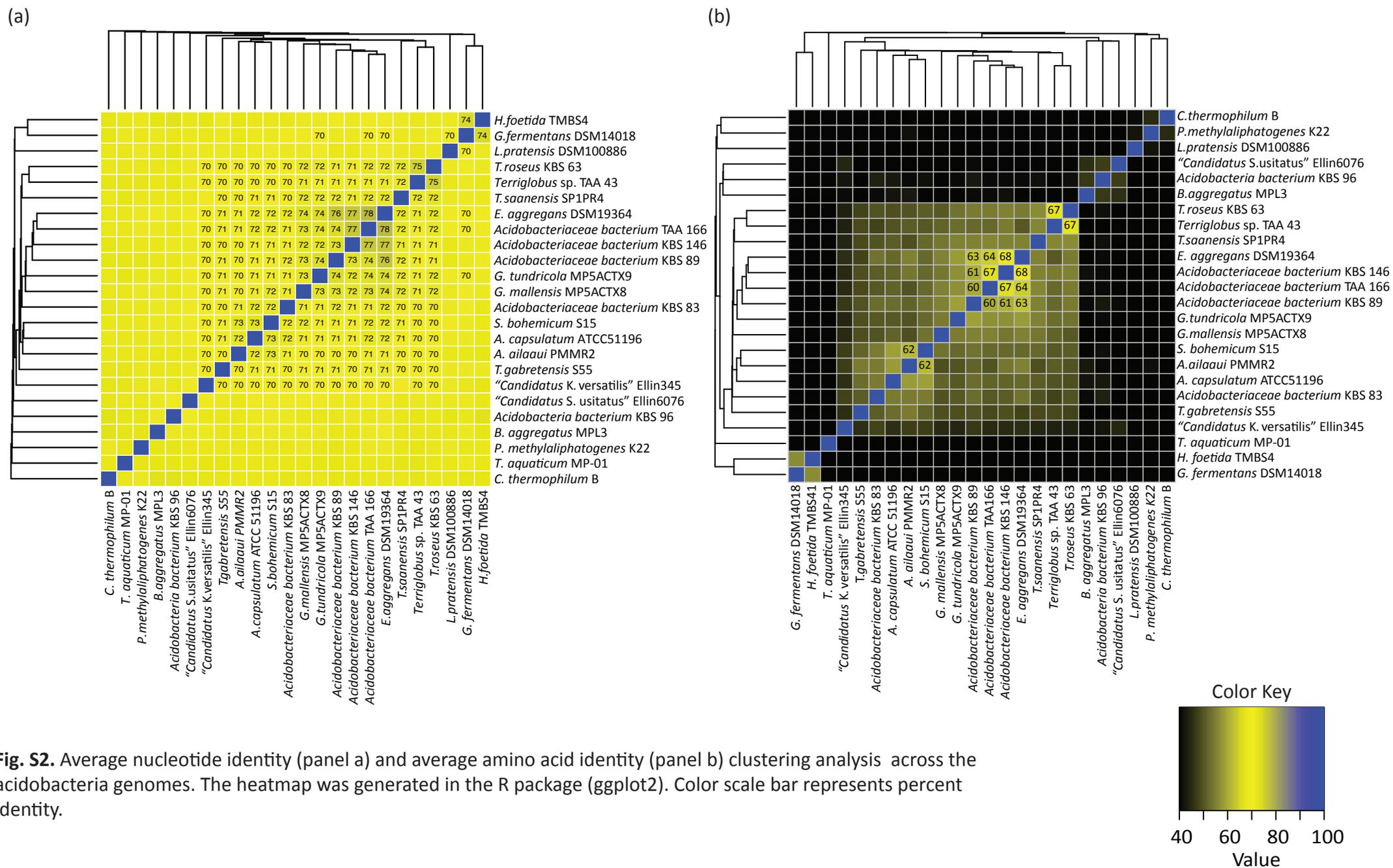


Fig. S1. Panel a depicts an acidobacterial 16S rRNA gene phylogenetic tree (ca. 1,248 nucleotides) of genomes retrieved in this study (8 taxa) and from publicly available genomes of cultivated strains (16 taxa), as inferred by maximum likelihood (RAxML), using the general time-reversible substitution model under the gamma model of rate heterogeneity (GTRGAMMA). Bootstrap support values (1000 iterations) are given on the branches of the tree. Genome assembly- and accession numbers, coordinates and accession numbers of the 16S rRNA genes are given in brackets. Numbers to the right of the tree correspond to the acidobacterial subdivisions. Scale bar indicates estimated nucleotide substitution per site. The root was placed on the branch leading to the *Actinobacteria*, belonging to the *Terrabacteria*. Panel b depicts the comprehensive phylogenomic tree (the part marked in grey is shown in Figure 2) by Bayesian inference based on a concatenated dataset of 43 universally conserved marker genes. The scale bar indicates 0.4 changes per nucleotide. Additional details can be found in Supporting Information.



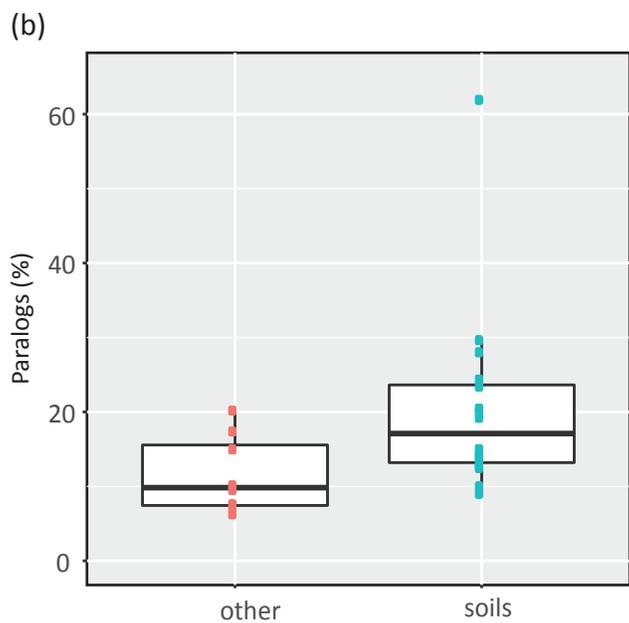
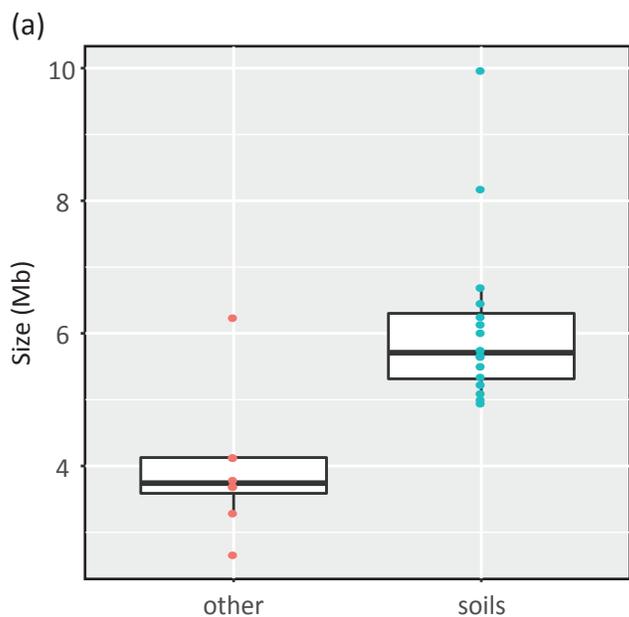


Fig. S3. Distribution of genome size (panel a) and percent of paralogous genes (panel b) across genomes stemming from “soils” and “other” environments. The percent of paralogous genes were normalized to gene count. The definition of “soil” vs “other” genomes can be found in Table S1. Data were obtained from the IMG JGI website.

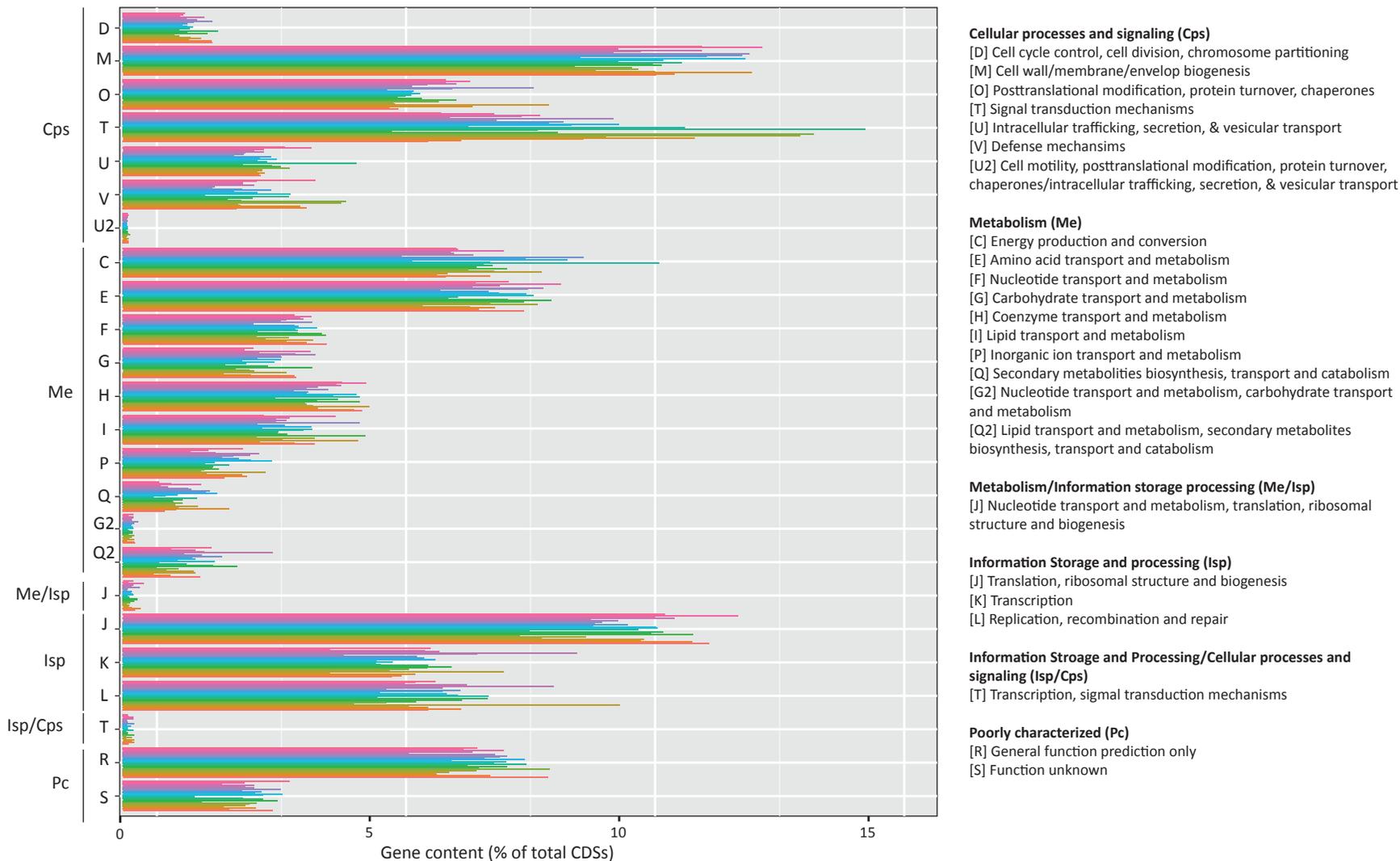


Fig. S4. Gene content by COG functional categories within the acidobacterial core genome. Each color represents a different genome. Functional categories are grouped by metabolism (Me), cellular processes (Cp), information storage and processing (Isp), and poorly characterized (Pc).

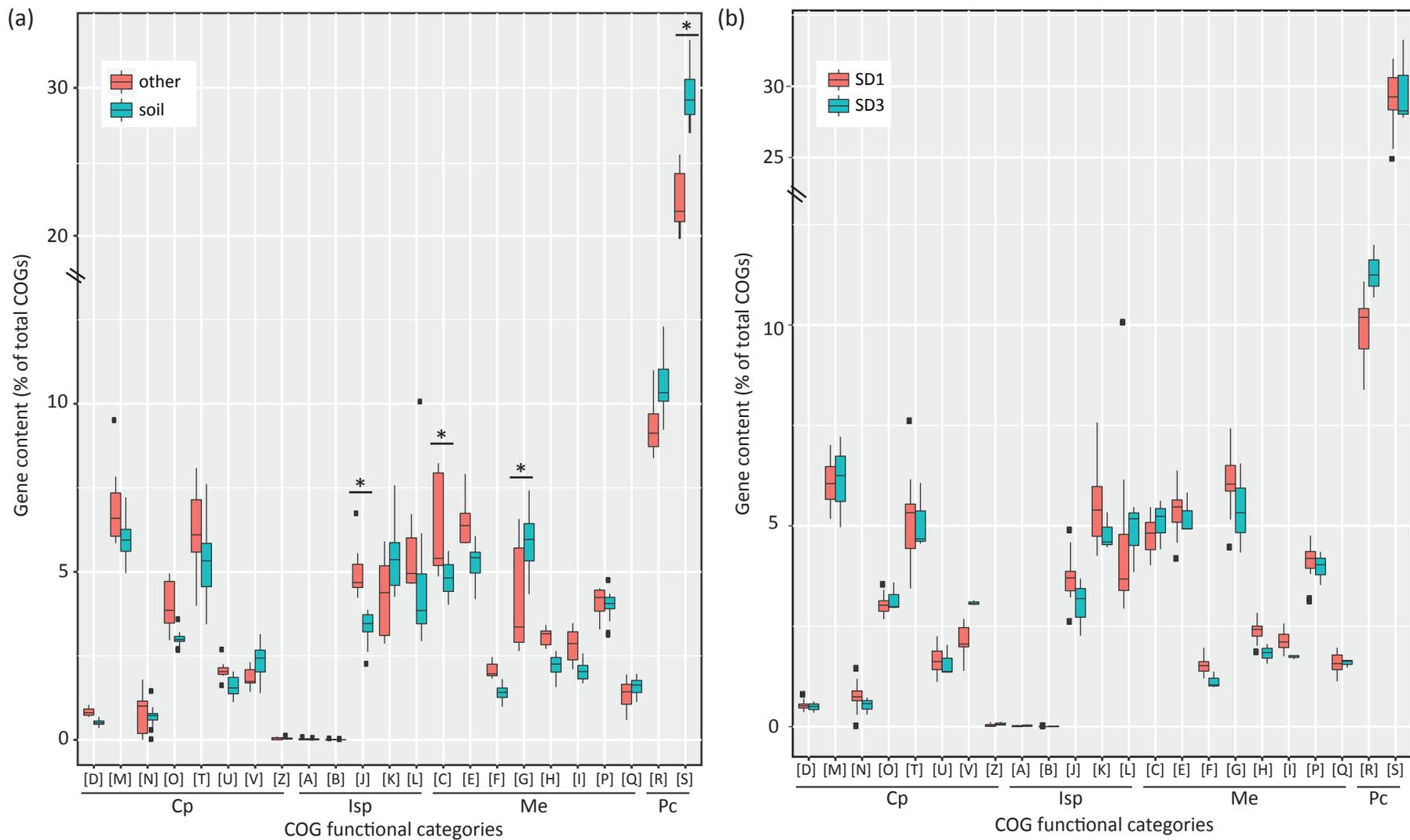


Fig. S5. Boxplot distribution of COG functional categories across environments (panel a) and subdivision 1 and 3 genomes (panel b). COG functional categories are grouped by cellular processes (Cp), information storage and processing (Isp), metabolism (Me) and poor characterized (Pc). The description of the sub-categories can be found in Fig. S3 and definition of “soil” vs “other” genomes can be found in Table S1. Asterisks depict significant differences based on a chi-square goodness of fit.

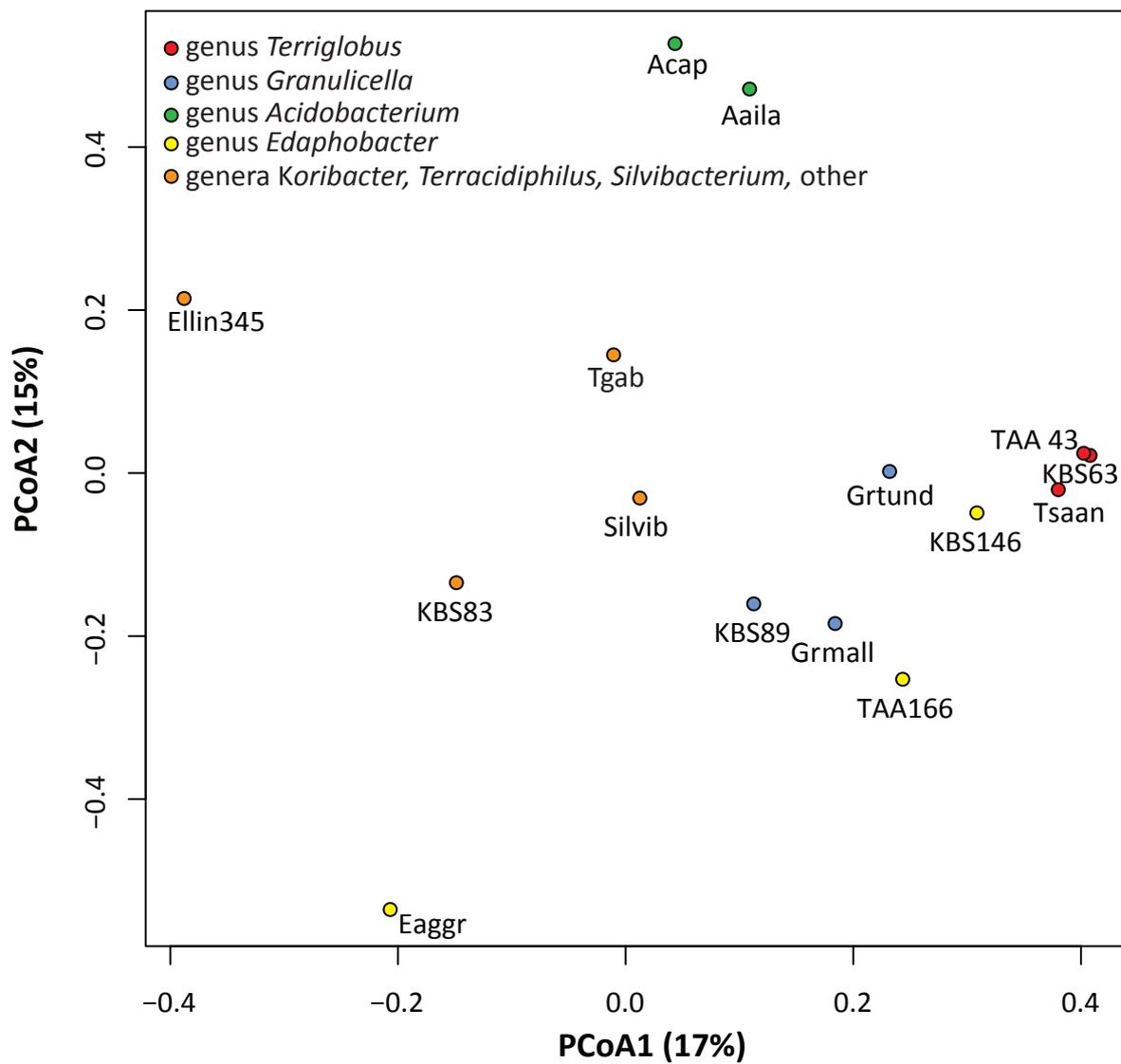


Fig. S6. PCoA plot based on the COG/NOGs of the genomes of genera from subdivision 1 based on the Bray–Curtis distance. The listed abbreviations for the genomes can be found in Table S1. Genera are depicted in different colors.

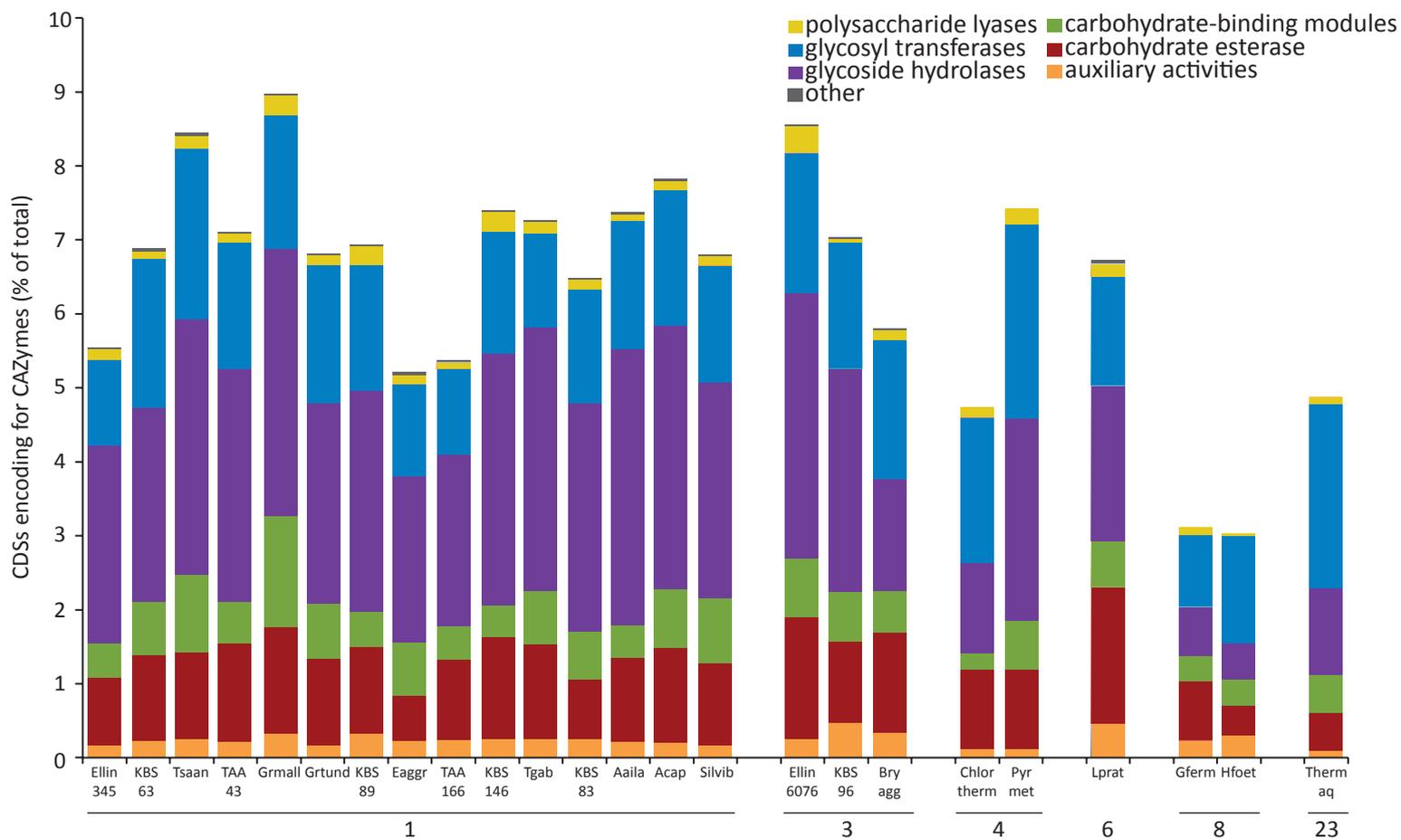


Fig. S7. Distributions of CDSs encoding for carbohydrate-active enzymes based on the database dbCAN (<http://csbl.bmb.uga.edu/dbCAN/index.php>), specifically depicting polysaccharide lyases, glycosyl transferases, glycoside hydrolases, carbohydrate-binding modules, carbohydrate esterase and auxiliary activities. "Other" denotes a sum of CDSs encoding for cohesion, dockerin and S-layer.



Fig. S8. Distributions of glycoside hydrolases (GH) amongst the acidobacterial genomes, separated by subdivisions based on the dbCAN (<http://csbl.bmb.uga.edu/dbCAN/index.php>). The GH family number is depicted on the right-hand side. Scale bar depicts the Z-scores for each GH family; the darker the color, the more putative CDSs in each respective genome were identified.

